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Listing first 45 summaries
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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G160_MOUSE
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US01_YEAST
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MYS2_AEQIR
TANA_XENLA
MYSB_CAEEL
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P50533 xenopus lae
Q9323 drosophila
P25386 saccharomyc
P08799 dictyosteli
P58302 thermoplasm
P24733 aequipecten
Q01550 xenopus lae
P02566 caenorhabdi
O08638 mus musculu
P33176 homo sapien
P35749 homo sapien
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P35749 oryctolagus
C29230 archaeoglob
P05659 acanthamoeb
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P42566 homo sapien
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P42566 homo sapien
P02567 caenorhabdi
P82094 homo sapien
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ALIGNMENTS	G160_HUMAN MYSP_BRUMA	MYSC_CHICK	MYH7_HUMAN	MYH7_MESAU	REST_HUMAN	XCPC_XENLA	MFP1_ARATH	MYSU_RABIT	MYHB_CHICK	мүн9_ниман
	Q08378 homo sapien Q01202 brugia mala	P/9293 Sus SCroid P29616 gallus gall	P12883 homo sapien	P13540 mesocricetu	P30622 homo sapien	P50532 xenopus lae	Q91w85 arabidopsis	099105 oryctolagus		P35579 homo sapien

RESULT

RP (5)  RP CHARACTERIZATION.  RX MEDLINE-98437347;  RA Chan G.K.T., Schaal  RT Characterization  RT interactions with 1  RI J. Cell Biol. 143:0  CC -!- FUNCTION: PROBLE  CC RETINOBLASTOMA  CC -!- SUBGELLULAR LOO			Eukaryota; M Mammalia; Eu NCBI_TaxID-9 [1] SEQUENCE FRO TISSUE-Breas MEDLINE-9534 Liao H., Win "CENP-F is a kinetochores	NE HUMAN CENE HUMAN CENE HUMAN P49454; Q132 01-FEB-1996 01-FEB-1996 16-CCT-2001 CENPF Kinet CENPF.
(5) CHARACTERIZATION. CHARACTERIZATION. MEDLINE=98437347; PubMed=9763420; CCHAR G.K.T., Schaar B.T., Yen T.J.; "Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBRI."; J. Cell Biol. 143:49-63(1998)i- FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLVED IN CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS WITH RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBRIi- SUBUNIT: HOMO- OR HETERODIMER.	domain sufficient for nuclear localization."; Biochem. Biophys. Res. Commun. 212:220-228(1995).  [4] [6] [6] [6] [7] [8] [9] [9] [9] [9] [9] [9] [9] [9] [9] [9	[2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=95379848; PubMed=7651420; MEDLINE=95379848; PubMed=7651420; Zhu X., Mancini M.A., Chang KH., Liu CY., Chen CF., Shan B., Jones D., Yang-Feng T.L., Lee WH.; "Characterization of a novel 350-kilodalton nuclear phosphoprotein that is specifically involved in mitotic-phase progression."; Mol. Cell. Biol. 15:5017-5029(1995). [3] MOL. Cell. Biol. 15:5017-5029(1995). SEQUENCE OF 2194-3210 FROM N.A. SEQUENCE OF 2194-3210 FROM N.A. MEDLINE=95336446; PubMed=7612011; Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.; "A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal departs and self-sitent for miclear localization."	Hound Suplens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBL_TaxID=9606;  [1]  SEQUENCE FROM N.A.  TISSUE=Breast carcinoma;  TISSUE=Breast carcinoma;  MEDLINE=95348175; PubMed=7542657;  Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;  MICRMP-F is a protein of the nuclear matrix that assembles onto kinetochores at late G2 and is rapidly degraded after mitosis.";  J. Cell Biol. 130:507-518(1995).	STANDARD; PRT; 3210 AA. 46; Q13171; (Rel. 33, Created) (Rel. 33, Last sequence update) (Rel. 40, Last annotation update) ochore protein (Centromere protein F) (Mitosin) (AH

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by non-profit institutions as long as its content is in
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DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE
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L -> Q (IN REF. 2).
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16-OCT-2001
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,
type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B).
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
              SEQUENCE FROM N.A. Ohara M., Ishiguro
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                                                                    Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                      NCBI_TaxID=9913;
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nonmuscle

myosin

chain

B mRNA,

complete cds.";

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                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                  NP_BIND
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                        Fram; FFU4/35; MyOSin_N; 1.
Pfam; PF01576; MyOSin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myOSin_head; 1
SMART. CMOONIE. TO
                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
Pfam;
 1198
                                               1138
                                                                                             1078
                                                                                                                                                                                                               Coiled coil; Alkylation; Multigene family.

DOMAIN

1 785

MYOSIN HEAD-L.

DOMAIN

786

815

10

DOMAIN

845

1976

COILED COIL ()

MP_BIND

178

185

ATP (DOTENTIAL)

MOD_RES

701

701

ALKYLATION (S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB022023; BAA36494.:
EMBL; U15716; AAA87715.1;
HSSP; P08799; 1LVK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1999)
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myosin heavy chain II-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95301542; PubMed-7782316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 204-302
                                                                                                                                                                                                                                                                                              Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                           PROSITE; PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Neuronal cell expression of inserted isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Itoh K., Adelstein R.S
                       88
                                                                     39
                                                                                                                4 INKLFFDLAQEEENV-------LDAEF--LKNELDSVKAQLSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
RQRHATALEELSEQLEQAKRFKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKL
                                          EKQKRDLSEELEALKTELEDTLDTTAAQQELRTKREQEVAELKKALEEETKSHEAQIQDM
                                                                   IDELKIQVAKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFESEKASRNKA 1137
                      PF00063; myosin_head; 1.
PF02736; myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      PF00612; IQ; 1
                                                                                                                                                                                                                                                                                                                      SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                   SM00015;
                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               p; IPR000048; IQ.
p; IPR004009; Mycsin_tail.
p; IPR0022017; Spectrin.
p; IPR001609; Mycsin_head.
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cortex
                                                                                                                                                                                                    A,
                                                                                                                                                                                                                                                                                                                                   IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAA36494.1; -.
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                                                                                                                                                    15.7%;
21.4%;
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                                                                                                                                                                                  IQ.
COLLED COIL (POTENTIAL).
ATP (POTENTIAL).
ATP (ATTION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
7 MW; 6144354451C0F790 CRC64;
                                                                                                                                           58;
                                                                                                                                        Score 169; DB 1; Length 1976;
Pred. No. 0.027;
8; Mismatches 87; Indels 9
                                                                                                                                                                                                                                                                         MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLE IN CYTOKINESIS, SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions on
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                                                                                                                                           ;86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHOWING
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RESULT
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Matches 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1318
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                DETECTABLE MALE ANTIGEN (SDM).

-! TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS.
FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO
LEYDIG CELLS, SPERMATOGONIA, OR SPERMATOCYTES.
-!- SIMILARITY: HIGH, TO HUMAN GOLGIN-160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Seq. 7:71-82(1997).
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR TESTIS DEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLOGICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoantigen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 male-enhanced antigen-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97217683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CD-1; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Golgin-160 (Male-enhanced antigen-2) GOLGA3 OR MEA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G160_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1374 TDTKKKVDD 1382
                                                                                                                                                                                                      Spermatogenesis; Developmental protein.
DOMAIN 201 204 POLY-ALA.
                                                                                                                                                                                                                                                   EMBL; D78270; BAA19612.1; HSSP; P18852; 1SCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kondo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P55937;
                                                                                                                                                                                                                                    MGD; MGI:96958; Golga3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and molecular characterization of cDNA encoding a male-enhanced antigen-2 (Mea-2): a putative family of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                          SEQUENCE
                                                         590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 -SEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYEN---
                           55
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                                                                                                                                                                                                                                                                                                                                                                                                                     INITIATOR.
                                                                            DLAQEEENVLDA-EFLKNE------LDSVKAQLSQKDREKR-------DSQAIIDTLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSLRKKSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDTQELLQEETRQKLNLSSRIRQ-LEEERSSLQEQQEEEEEAR---RSLEKQLQALQAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAQVQELHAKVSEGDRLRVELAEKANKLQNELDNVSTLLEEAEKKGIKFAKDAAGLESQL
DLAVKSNQVEHLQQE-----TATLRKQMQKVKEQFVQQKVMVEAYRRDATSKDQLINE
                          TLEERNATVESLQNALNKAEMLCSTLKKQM----KFLEQ-----RQDET-----KQ
                                                       ELQREADSREDAIHFLQNEKIVLEVALQSAKSDKEELDRGARRLEEDTEETSGLLEQLRQ
                                                                                                                 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutou S.;
                                                                                                                                                                                          201 21
1325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9063644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELADRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEI
                                                                                                                               15.7%;
                                                                                                                                                                                          149880 MW;
                                                                                                                  50;
                                                                                                                 Score 168.5; DE Pred. No. 0.019; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                          3230636962C687B0 CRC64;
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(MEA-2).
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                                                                                                                  84;
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                                                                                                                  Indels
                                                                                                                                             Length 1325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . TRANSCRIPTS CAN EXPRESSION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                   OR MET-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y a mouse
ne Golgi
                                                                                                                  87;
                                                                                                                                                                                                                                                                                                                                                                                      collaboration
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                                                                                                                 Gaps
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XCRE_XENLA
ID XCRE
AD 101-OCT
DT 01-OCT
DT 01-OCT
DT 15-JUL
DE CAMPAIN
OC ENWARY
OC AMPAIN
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RN [1]
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RN SEQUEN
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RT Conder
RY MITTON
RN HIST
DR HIST
DR Pfam;
RW Mitos
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                                                   Query Match
Best Local
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                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                     NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XCPE_XENLA
P50533;
                                                                                                                                                                                                                                                                                              modified and this st
entitles requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   condensation in vitro.";
Cell 79:449-458(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosome assembly protein XCAP-E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
                                                                                                     SEQUENCE
                                                                                                                                                                                                                  InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A heterodimeric coiled-coil protein required for mitotic chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hirano T., Mitchison T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95042742; PubMed=7954811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    763
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               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                  MITOTIC CHROMOSOMES.
SUBUNIT: ASSOCIATES WITH XCAP-C PROBABLY AS HETERODIMER.
SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN
MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND
MITOTIC EXTRACTS. THERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.
DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: REQUIRED FOR
EFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKEMKTKHKAYENAVSILSRRLQEALASKEATDAELNQLRAQSTGGSSDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AREEAHRLKCKMKTMEQIELLLQSQRSEVE----EMIRDMGVGQSAVEQLAVYCVSLKKE
                                                                                                                                                                                                                                           U13674; AAA64680.1;
P07751; 1AJ3.
                                                                                                                                                                                         PF02483; SMC_C;
PF02463; SMC_N;
                                                   Similarity
                                                                                                                                                                                                                                                                                                         non-profit institu
                                                                                                                                                                             ATP-binding;
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus
                                                                                          356
356
513
1032
1121
3 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                          Latement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                     institutions as long as its content
                                                15.6%;
                                                                                                     136341
                                                                                                                                                                              Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LKEA----RKATGELADRLKKDLVSSRSKLKTLNTELDQA
                                       45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOTH ASSEMBLY AND
                                                                                                   ed coil; Nuclear protein.
ATP (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
ALA/ASD-04323DD0027DF309 CRC64;
                                      Score 167.5;
Pred. No. 0.02
$5; Mismatches
                                                                                                     ₩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1
PROSITE; PS50096; IQ; 1
Myosin; Alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994
01-JUN-1994
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PTODOm; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as modified and this statement is not removed. Use the entities requires a license agreement (See htter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYSN_DROME Q99323;
                                                                                                                                                                                                      InterPro; IPR002928;
InterPro; IPR001609;
Pfam; PF00612; IQ; 1
                                                                                                                                                                                                                                                                                  FlyBase; FBgn0005634;
InterPro; IPR000048; I
                                                                                                                                                                                                                                                                                                                                                     PIR; A36014; A36014.
PIR; B36014; B36014.
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M35012; AAA28713.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
MEDLINE=90349606; PubMed=2117279;
                                                                                                                                                                                                                                                                     InterPro; IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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rnative splicing; Co
Calmodulin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
chain, non-muscle (Zipper protein) (Myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TTYKQQIETVDEAMKAYQEQADSMASEVSKNKEAVKKAQDELAKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                          Myosin_tail.
myosin_head.
                                                                                                                                                                                                                                                                     Myosin_N.
                     Coiled
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                     coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no rest
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                   Actin-binding
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tail and differential
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Best Local S
Matches 61
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USO1_YEAST
P25386;
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DOMAIN
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DOMAIN
    SECULINAL C. Symington L.S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
Submitted (MAY-1996) FOR PROTEIN TRANSPORT FROM THE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1492
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation Intracellular protein transport protein USO1 OR INTI OR YDL058W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1432
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                                                                               SEQUENCE OF 1-8 FROM N.A.
                                                                                                                       Submitted (FEB-1993)
                                                                                                                                         Kendrick K.E
                                                                                                                                                          Hostetter M.K.,
                                                                                                                                                                                 SEQUENCE OF
                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                  MEDLINE-91185402; PubMed-2010462;
Nakajima H., Hirata A., Ogawa Y.,
                                                                                                                                                                                                                                                                                                                                                STRAIN-X2180-1A;
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                                                                                                                                                                                                                                                                                     Yamasaki M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLGLSSKLRQIESEKEALQEQLEEDDEAKRNY---ERKLAEVTTQMQEIKKKAEEDADLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LKCKMKTMEQIELLLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEAR
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                                                                                                                                                                                                                  transport in Saccharomyc Biol. 113:245-260(1991).
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859
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2017
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                                                                                                                                                                                                                                         Saccharomyces cerevisiae
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transport protein USO1.
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                                                                                                                                                            D.J.,
                                                                                                                         the
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COILED COIL (POTENTIAL).
ATP.
25 KDA/50 KDA JUNCTION.
50 KDA/20 KDA JUNCTION.
ACTIN-BINDING.
REACTIVE SULFHYDRYL/ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
                                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 166; DB Pred. No. 0.04; Mismatches
                                                                                                                                                            Bendel C.M., McClellan M.,
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MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGHT MEROMYOSIN (LMM).
ALPHA-HELICAL TAILPIECE (LMM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                  Yonehara T., Yoda K.,
                                                                                                                                                                                                                                            is required cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1790
                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces
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                                                                                                                    databases
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OC COC

MHCA.

Eukaryota;

Dictyostelium discoideum (Slime mold)

Mycetozoa; Dictyosteliida; Dictyostelium

Myosin

II heavy

chain,

non

muscle

01-NOV-1988 01-OCT-1989 16-OCT-2001

Rel. 09, Create (Rel. 12, Last s (Rel. 40, Last a

sequence update) annotation updat

update)

Created)

P08799; MYS2\_DICDI

STANDARD;

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2116

A

MYS2\_DICDI

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                                                                Qγ
RESULT
                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X54378; CAA38253.1; -.
EMBL; L03188; AAB00143.1; -.
EMBL; U53668; AAB6659.1; -.
PIR; A38455; A38455.
HSSP; P80220; IDIP.
SGD; S0002216; US01.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                    1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                        1580
                                                                                             1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinform
the European Bioinformatics Institute. The
use by non-profit institutions as long
                                                                                                                                                                                                        1424 ELLEEKQNTIKS--LQDEI-----LSYKDKITRNDEKLLSIERDNKRD----LESLKEQ
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                184 LNTELDQAKLELRSAQKDLQSADQEITSLRKKSDD
                                                                                                                                                                              70
                                                                                                                                                                                                                                 10 DLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.

ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COLLED COLLED COLLED CORM FILLMENTOUS STRUCTURES IN THE CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE
                                      SGSELETVKQELNNAQEKIRINAEENTVLKSKLED
                                                                                             ETIRKSDEKLEQ-----SKKSAEEDIKNLQHEKSDLISRINESEKDIEELKSKLRIEAK
                                                                                                                      RDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRL---KKDLVSSRSKLK---T
                                                                                                                                                 LRAAQESKAKVEEGLKKLEEESSKEKAELEKSKEM-----MKKLESTIESNETELKSSM
                                                                                                                                                                            LNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRSEVEEMI
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                               725
465
991
1172
847
924
1253
1319
1461
1581
1581
1600
1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein transport;
                                                                                                                                                                                                                                                                                                                                   1790
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                      725 1790
165 487
191 1790
72 1790
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14 1253
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1 1319
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1772
A; 206424 P
                                                                                                                                                                                                                                                                           15.2%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spectrin
                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                            G -> E (IN REF. 2).
E -> K (IN REF. 2).
V -> I (IN REF. 2).
I -> V (IN REF. 2).
N -> S (IN REF. 2).
G -> S (IN REF. 2).
I -> V (IN REF. 2).
I -> V (IN REF. 2).
D -> DEEDDEE (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                WW;
                                                                                                                                                                                                                                                             Score 163; DB 1
Pred. No. 0.052;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISPENSABLE FOR THE ASP/GLU-RICH (ACIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOlgi stack; Cytoskeleton; GLOBULAR HEAD.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Bioinformatics
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                                      1614
                                                                                                                                                                                                                                                                                        DB 1;
                                                                  218
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                                                                                                                                                                                                                                                              77;
                                                                                                                                                                                                                                                                                     Length 1790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN
                                                                                                                                                                                                                                                                                                                                CRC64;
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                                                                                                                                                                                                                                                             30;
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Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;

"X-ray crystal structure and solution fluorescence characterization
of Mg.2'(3')-O-(N-methylanthraniloy1) nucleotides bound to the
Dictyostellum discoideum myosin motor domain.";
J. Mol. Biol. 274:394-407(1997).

-i- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY ACTIN.
ACTIVITY THAT IS ACTIVATED BY ACTIN.
-i- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES
INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKAL
LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) MEDLINE-98070605; PubMed-9405148;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gulick A.M., Bauer C.B., Thoden J.B., Rayment I., "X-ray structures of the MgADP, MgATPgammaS, and MgA of the Dictyostelium discoideum myosin motor domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) MEDLINE=97452580; PubMed=9305951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE=96206189; PubMed=8611530;
Smith C.A., Rayment I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) MEDLINE=95345066; PubMed=7619795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Warrick H.M., de Lozanne A., Leinwand L.A., Spudich J.A.; "Conserved protein domains in a myosin heavy chain gene f Dictyostelium discoideum.";
                                                <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "X-ray structure of the magnesium(II).ADP.vanadate complex of the Dictyostelium discoideum myosin motor domain to 1.9-A resolution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II)-pyrophosphate truncated head of Dictyostelium discoideum myosin to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) MEDLINE-95345067; PubMed-7619796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium myosin heavy chain."; FEBS Lett. 227:71-75(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphorylatable heavy chain fragment of Dictyostelium myosin FEBS Lett. 269:239-243(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "X-ray structures of the myosin motor domain of Dictyostelium discoideum complexed with MgADP.BeFx and MgADP.AlF4-."; inchemistry 34:8960-8972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88112226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87092266; PubMed=3540939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 34:8973-8981(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fisher A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88112226; PubMed-2828113;
Wagle G., Noegel A., Scheel J., Gerisch
"Phosphorylation of threonine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90353583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lueck-Vielmeter
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                                         CORTEX.

DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO
  MEROMYOSIN
SPLIT INTO
                                                                                       SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n discoideum myosin motor 35:5404-5417(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                          36:11619-11628(1997)
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  (LMM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=2387408;
                         AND
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  SUBFRAGMENTS
                                                                                     HIGHEST CONCENTRATION IN
HEAVY MEROMYOSIN SUBFRAGMENTS (S1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grabatin B.,
                                                                                                                                                                                                                                                                                                                                                                              OF.
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cloned
  AND
                         (MMH)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sutoh K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MgAMPPNP complexes
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ROD-SHAPED
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                                                                                       THE POSTERIOR
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                                                                                                                                   (MHC), 2 ALKAL:
CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resolution.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from
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                                                                                                                                                        ALKALI
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61

ATVESLQN---

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ALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKC

В δÃ

852

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NKLFFDLAQEEENVLDAE-FLKNELDSVKAQLSQKD---REKRDSQAIIDTLRDTLEERN

DKLEKSLKDTESNYLDLQRQLKAEKETLKAMYDSKDALEAQKRELEIRVEDMESELDEKK

911 60

106

Query Ma Best Loc Matches

Match Local :

l Similarity 67; Conserv

Conservative

52;

Mismatches

; 88 1,

Indels Length

63;

Gaps

11;

15.1%; 25.0%;

Score 162.5; Pred. No. 0.

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107

KMKTMEQIELLLQSQRSEVEEMI - - -

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-GQSAVEQLAVYCVS--

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MOD_RES
MOD_RES
MOD_RES
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SEQUENCE
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PDB; 1MMD;
PDB; 1MMG;
PDB; 1MMD;
PDB; 1MND;
PDB; 1MNE;
PDB; 1VOM;
PDB; 1VVK;
                                                                                                                                                 NP_BIND
                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR001609; myosin_he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
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                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                        Calmodulin-binding; Methylation;
                                                                                                                                                                                                                                                                              Myosin;
                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DictyDb; DD01008; mhcA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                 DOMAIN
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                               ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFRAGMENT (S2).

BOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPT CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

PYM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION IF ACTIVITY ACTIVATED ATPASE ACTIVITY.

MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ACTIVITY, PERRAPS CORRELATED WITH THE ABSENCE OF A CYS ACCITATION, 1688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSITION (688).
                                                                                                                                                                                                                                                                                                                                                                                                   PF00063; myosin_head; 1. PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M14628;
                                                                                                                                                                                                                                                                                                                   SM00015; IQ; 1.
SM00242; MYSc;
                                                                                                                                                                                                                                                                            ; PS50096; IQ; Coiled coil; /
                                                                                                                                                                                                                                                                                                                                                           PR00193; MYOSINHEAVY
PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-DEC-97.
17-AUG-96.
03-DEC-97.
03-DEC-97.
17-AUG-96.
17-AUG-96.
23-DEC-96.
23-DEC-96.
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Methylation; Alkylation; Phosphorylation.
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METHYLATION (DI-) (POTENTIAL).
ALKYLATION (SH-1).
PHOSPHORYLATION (BY MHCK).
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PHOSPHORYLATION (BY MHCK).
PHOSPHORYLATION (BY MHCK).
W; 2FC3770BB1EE56A1 CRC64;
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RESULT 9
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Rawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
-i-FUNCTION: Involved in DNA double-strand break repair (DSBR). The strange of the s
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA double-strand break repair rad50 ATPase
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repair; Hydrolase; ATP-binding;
BIND 30 37 ATP (B
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TY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
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                                                                                                                                                                                                                         -i- FUNCTION: MUSCLE CONTRACTION.
-i- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
-i- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS MLC-2).
-i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-i- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-i- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure of the regulatory domain of scaresolution: implications for regulation.";
Structure 4:21-32(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chain. Sequence comparison with other heavy chains reveals
that might be critical for regulation.";
J. Biol. Chem. 266:18469-18476(1991).
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"Structure of the regulatory
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MEDLINE=94173332; PubMed=8127365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MEDLINE=96419133; PubMed=8805510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Adductor muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92011595; PubMed=1917970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pectinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Bivalvia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aequipecten irradians (Bay scallop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myosin heavy chain, striated muscle.
                                                                                                                  the European
                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houdusse A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368:306-312(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xie X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91088319; PubMed=2263488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nyitray L., Goodwin E.B., Szent-Gyoergyi A.G.;
Complete primary structure of a scallop striated muscle myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                             SWISS-PROT entry is copyright.
een the Swiss Institute of Bioi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harrison D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 21, Created)
(Rel. 21, Last seq
(Rel. 40, Last ann
                                                    ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cohen C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pectinidae; Argopecten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohen C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schlichting I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence up
annotation
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Best Local S
Matches 73
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InterPro; IPRO04009; Myosin_tail.
InterPro; IPRO02928; Myosin_tail.
InterPro; IPRO029217; Spectrin.
InterPro; IPRO01609; myosin_head.
Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF002736; Myosin_head; 1.
Pfam; PF02736; Myosin_tail; 1.
                                                   TANA_XENLA
Q01550;
Q1-JUN-1994
Q1-JUN-1994
16-QCT-2001
                                                                                                         XENLA
                                                                                                                                                                                                                                                                                                                                                                                                              TURN
SEQUENCE
           Tanabin.

Yanabin.

Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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MOD_RES
MOD_RES
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HELIX
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DOMAIN
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ATP-binding;
   Xenopodinae;
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A40997;
                                                                                                                                                           MLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMK-----TMEQIELLLQSQRSEVEEMI 129
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                                                                                                                                                RELEELGERLDEAGGATSAQIELNKKREAELLKIRRDLEEASLQHEAQISALRKKHQD
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SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muscle
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(Rel.
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A40997
   Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96; 10; 1.
protein; Coiled coil; Thick filament; protein; Colled coil; Thick filament; Lkylation; Calmodulin-binding; 3D-struc 1777 MYOSIN HEAD-LIKE.
                                                                                              STANDARD;
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ATP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIMI ALKYLATION (SH-2) (BY SIMI
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Pred. No. 0.064;
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SIMILARITY)
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Best Local S
Matches 57
                                  MYSB_CAEEL
P02566;
21-JUL-1986
21-JUL-1986
16-OCT-2001
                                                                                                   _CAEEL
          Myosin heavy chain B (MHC B). UNC-54 OR MYO-4.
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SEQUENCE
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DOMAIN
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DOMAIN
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PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M99387; AAA49966.1; PIR; JH0720; JH0720. InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=92398961; PubMed=1524825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuron 9:417-428(1992).
-!- TISSUE SPECIFICITY: GROWTH CONES OF -!- DEVELOPMENTAL STAGE: IS EXPRESSED I DURING EMBRYOGENESIS IN THE BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hemmati-Brivanlou A., Mann R.W., Harland R.M.; "A protein expressed in the growth cones of embryonic vertebrate neurons defines a new class of intermediate filament protein.";
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                  WQGAVEEYKSEVSVLEAGLSESKENLRKVLEENKQNRLLLQSLDKELVSLKMRKE
                                                                                                                                                                           LKKDLVSSRSKLKTLNTELDQAKLELRSAQKD-----LQSADQEITSLRKKSD
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57; Conserv
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                                                                                     STANDARD;
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24.38;
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TAIL.
COLL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
COIL 2A.
LINKER 2.
COIL 2B.
COIL 2B.
COIL 2B.
                                                                                                                                                                                                                                                                                                                                                    Score 160.5;
Pred. No. 0.07
58; Mismatches
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D IN THE NEURULA AND PERSIST
N, CRANIAL NERVES, AND SPINAL
                                   update)
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EMBL; J01050; AAA28124.1; -.
EMBL; V01494; CAA24738.1; -.
PIR; A02992; MWKW.
HSSP; P08799; IMND.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                            This SWI
between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=83273600; PubMed=6576334;
Karn J., Brenner S., Barnett L.;
"Protein structural domains in the Caenorhabditis elegans unc-54
myosin heavy chain gene are not separated by introns.";
Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; M
Rhabditidae;
                                                                                                                         PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_heac
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"The genes su
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                                                                            ATP-binding;
                                                                                            SMART; SM00242; MYSc;
Myosin; Muscle protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82272395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFRAGMENT (S2).

MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS C.ELEGANS.

MISCELLAPOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE MISCELLAPOUS. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOWAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PYM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: MÜSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS
HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MAC-2).
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes sup-7 X and sup-5
                                                                                                                                                   PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33:575-583(1983)
                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                           non-profit institu
and this statement
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                                                                             Methylation;
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PubMed=7202124;
                                                                                                                        myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                      preatics Institute. There are no rest
institutions as long as its content
institutions as long as its content
tarement is not removed. Usage by a
                                                                         Coiled coil; Thick filament; Acn; Alkylation; Multigene family.
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                             MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL)
ALPHA-HELICAL TAILPIECE
                ALPHA-HELICAL
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er RNA.";
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                                                  MIDLINE-96172919; PubMed-8593698;
MEDLINE-96172919; PubMed-8593698;
Suzuki T., Kim H.S., Kurabayashi M., Hamada H., Fujii H., Aikawa M., Watanabe M., Watanabe N., Sakomura Y., Yazaki Y., Nagai R.;
Watanabe M., Watanabe N., Sakomura Y., Yazaki Y., Nagai R.;
"Preferential differentiation of P19 mouse embryonal carcinoma cells "Preferential differentiation of P19 mouse embryonal carcinoma cells into smooth muscle cells. Use of retinoic acid and antisense against into smooth muscle cells. Use of retinoic acid and antisense against into smooth muscle cells. Use of retinoic acid and antisense against into smooth muscle cells.
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the central nervous system-specific
Circ. Res. 78:395-404(1996).
-!- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                      MEDLINE-95008063; PubMed-7923625;
Miano J.M., Cserjesi P., Ligon K.L., Periasamy M., (
"Smooth muscle myosin heavy chain exclusively marks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97242182; PubMed-9125171;
Hasegawa K., Arakawa E., Oda S., Matsuda
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STRAIN-BALB/C; TISSUE=Uterus;
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Mammalia; Eutheria;
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ALKYLATION (SH-2).
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밁
                           Q
                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF002736; Myosin_v; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF00193; MYOSINHEAVY.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM000142; MYSC; 1.
 1688
                                                                                                                                CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-: SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

-: ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

-: DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

-: PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUITED FOR WOSIN ATPASE ACTIVITY.

-: MISCELLANEOUS: EACH WOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                               Myosin; Muscle protein; Coiled coil; To Calmodulin-binding; ATP-binding; Methy Multigene family; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD;
                                                                                                                                                            CONFLICT
                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                        VARSPLIC
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                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                             NP_BIND
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                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLIT FURTHER INTO 2 SUBFRAGMENT (S2).
                           DLAQEEENVLDAEFLKNELDSVKAQLSQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:1
DLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNTLQDEKRRLEARIAQLEEELEE 1747
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D85924;
L25860;
S81516;
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                                                                        Similarity
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661
762
129
701
711
1930
                                                           Conservative
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1934
1972
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776
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161
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                                                                                                                            METHYLATION (TRI-) (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

RGNEASFVPSRRAGGRRVIENTDGSSEEMDARDSDFNGTKA
SE -> GPPPQETSQ (IN ISOFORM 2).

N -> D (IN REF. 3).
A -> V (IN REF. 2).
Q -> K (IN REF. 2).

Q -> K (IN REF. 2).
                                                        Score 160; DE
Pred. No. 0.08
53; Mismatches
                                                                                                                                                                                                                                                             ATP (POTENTIAL).
ACTIN-BINDING (E
ACTIN-BINDING (E
                                                                                                                                                                                                                                                                                                                     IQ. COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                         CARBOXYL-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                   MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                           pil; Thick filament; Actin-binding;
Methylation; Alkylation;
                           -----DREKRDSQAIIDTLRDTLEE
                                                                     DB 1.084;
                                                                                                                                                                                                                                                             (BY SIMILARITY). (BY SIMILARITY).
                                                                                   1.
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                                                        Indels
                                                        48;
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KINH, HUMAN
ID KINH, HUMAN
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AC P33176
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                                                                                                                                                                                                                                                                                                                                                    exclusively in neurons.";
Neuron 12:1059-1072(1994).

-i- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
-PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.

-i- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KINH_HUMAN P33176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kull F.J., Sablin E.P., Lau R., Fl "Crystal structure of the kinesin similarity to myosin.";
Nature 380:550-555(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY
MEDLINE-94242426; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Niclas J., Navone F., Hom 
"Cloning and localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96195066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interaction of the COOH-terminal domain with cytoplasmic in transfected CV-1 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Navone F., Niclas J., Ho
McCaffrey G., Vale R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92299683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell Biol. 117:1263-1275(1992).
                                                                                                                                    AND THE PROCESSES IN THE NEURONS.

TISSUE SPECIFICITY: FOUND IN NEWBORN AND ADULT BRAIN, LIVER, KIDNEY, SPLEEN, HEART, LUNG AND SCIATIC NERVE.

RIDNEY, SPLEEN, HEART, LUNG AND SCIATIC NERVE.

DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH
                                                                                                                                                                                                                                                                                                                     SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS.
SUBCELLULAR LOCATION: UNIFORMLY DISTRIBUTED
                                                                                            INTERACTS WITH OTHER PROTEINS (SUCH AS VESICLES AND MEMBRANOUS ORGANELLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKAKLKSTVAALEAKIAQLEEQVEQEAREK---QAATKSLKQKDKKLKEVLLQVEDERK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MAEQYKEQAEKGNTKVKQLKRQLEEAEEESQCINANRRKLQRELDEATESNEAMGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and expression of a human kinesin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7, Last sequence update)
0, Last annotation update)
(Ubiquitous kinesin heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -Booher N., Vale R. of a conventional
                                                                      THE
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                                                                      KINESIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fletterick R.J., Vale R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              motor domain reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sparks L., Bernstein H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       963
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kinesin motor expressed
                                                                      PROTEIN FAMILY.
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                                                                                                                   KINESIN
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                                                                                                                   LIGHT
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                                                                      KINESIN
                                                                                                                   CHAINS
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Matches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KIRESIN_MOTOR_DOMAIN2; 1.
MOTOR protein; Microtubules; Application of the Motor protein; Microtubules; Microtubules; Coiled DOMAIN 1 256 KINESIN-MOTOR.
DOMAIN 329 914 COILED COIL.
DOMAIN 315 963 GLOBULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                  MEDLINE-9942570; PubMed-10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell Eichler E.E., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA: human chromosome 16p and 16g.";
                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Myosin heavy chain, smooth muscle isoform (
MYH11 OR KIAA0866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO01752; kinesin. Pfam; PF00225; kinesin; 1. PRINTS; PR00380; KINESINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A41919;
PDB; 1BG2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
              SEQUENCE OF 1-1266 FROM N.A. TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                            MYHB_HUMAN STANDARD; P: P35749; 000396; P78422; 094944;
                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
 MEDLINE=99156230;
                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=99425270;
                                                                                                                                                                                                 NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602809;
                                                                                                                                                                                                                                                                                                                                                                                                                KKRQLEESVDALSEELVQLRAQEKVHEMEKEHLN-KVQTANEVKQAVEQQIQSHRE
                                                                                                                                                                                                                                                                                                                                                                                                                                         ARKATGELADRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMKSEVKTMVKRCKQLESTQTESNKKMEENEKELAACQLRISQHEAKIKSLTEYLQNVEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLKCKMKTM----EQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALNK------AEMLCSTLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DASKEEVKEVLQA-----LEELAVNYDQKSQEVEDKTKEYELLSDELNQKSATLASIDA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X65873; CAA46703.1;
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57; Conser
                                                        60:295-308(1999).
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 PubMed=10048485;
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muscle isoform (SM
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Pred. No. 0.046;
8; Mismatches
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                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P (BY SIMILARITY).
A1FE5760C3250C8B
                                                                                                                                                                                                                                                                                                                                          1972
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                                                                                                                                                                                                                                                                      (SMMHC)
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                                                                                  of DNA sequence
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C: FUNDUNT: MUSCLE CONTACTION:

CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC : SUBCELLUAR LOCATION: Thick filaments of the myofibrils.

CC :- TISSUE SPECIFICITY: SMOOTH MUSCLE; EXPRESSED IN THE UMBILICAL ARTERY, BLADDER, ESOPHAGUS AND TRACHEA.

CC :- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CC CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

CC -- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY CC PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY CC INVERSION INV(16)(P13022), PRODUCES A FUSION PROTEIN THAT CONSISTS OF THE 165 N-TERNINAL RESIDUES OF CBB-BETA (PEDB2) WITH THE TAIL CC REGION OF MYHIL THIS REARRANGEMENT IS ASSOCIATED WITH ACUTE MYELOID LEUKEMIA OF M4EO SUBTYPE.

CC MYELOID LEUKEMIA OF M4EO SUBTYPE.

CC MYELOID LEUKEMIA OF M4EO SUBTYPE.

CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED CC SUBTRAGMENT (S2).

CC -- SIMILARITY: CONTAINS 1 NYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                         Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences in vitro.";
                                                                                                                                                                         InterPro; IPR002928;
InterPro; IPR002017;
InterPro; IPR001609;
                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. Thuse by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yanagisawa M., Masaki T.,
"Human smooth muscle myosi
           Myosin; Muscle protein; Coiled c
Calmodulin-binding; ATP-binding;
                                                                                                                                                          Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: MUSCLE CONTRACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93263189;
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                                                                                                                                                                                                                                                       L; AF001548; AAC31665.1; -.
L; U91323; AAC35212.1; -.
L; AB020673; BAA74889.1; -.
L; D10667; -; NOT_ANNOTATED_CDS.
L; X69292; CAA49154.1; -.
P; P08799; IMMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                             160745;
                                            ; PD000355; myosin_head;
SM00015; IQ; 2.
SM00242; MYSC; 1.
E; PS50096; IQ; 1.
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R., Yoshida M.C., Furutani
wa M., Masaki T., Takao A.;
                                                                                                                                                                                                                          IPR000048;
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                            Coiled coil; Thick filament; Actin-binding;
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family; Proto-oncogene;

Methylation; Chromosomal

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Best Local
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                                                                                                         gene:
                                                                                                                                                                                     WYHII.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                    NYHB_RABIT STANDARD; PRT; 1972 AA p35748; Ol-JUN-1994 (Rel. 29, Created) Ol-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
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CONFLICT
SEQUENCE
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                    Myosin heavy MYH11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                          MEDLINE=92073350; PubMed=1961735;
Babij P., Kelly C., Periasamy M.;
"Characterization of a mammalian smooth muscle myosin heavy-chain
                                                                                                                                                                                                                                                                                                                                                              1921
                                                                                                                                                                                                                                                                                                                                                                                                          1864
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                                                                                                                                                                 SEQUENCE FROM N.A.
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e: complete nucleotide and protein coding sequence and analysis of 5' end of the gene.", c. Natl. Acad. Sci. U.S. A. 88:10676-10680(1991).

FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MIC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                             VNALKSK 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLAQEEENVLDAEFLKNELDSVKAQLSQK------DREKRDSQAIIDTLRDTLEE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQGNMEAMSDRVRKATQQAEQLSNELATERSTAQKNESARQQLERQNKELRSKLHEMEGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRRLEARIAQLEEELEE 1747
                                                                                                                                                                                                                                                                                                                                                                                    ITSLRKK
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ALKYLATION (SH-2) (POTENTIAL).
EEK -> NSE (IN REF. 3).
ELOS -> TLSF (IN REF. 2).
T -> S (IN REF. 3).
KQ -> NE (IN REF. 3).
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Pred. No. 0.09
52; Mismatches
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ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL)
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> L (IN REF. 3).
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SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are use by non-profit institutions as long as its a modified and this statement is not removed. Usage entities requires a license agreement (See http://w
  1921 VNALKSK 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin; Muscle protein; Coiled coil; Thick filament; Acti
Calmodulin binding; ATP-binding; Methylation; Alkylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00612; IQ; 1
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InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
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                                                                                          ---MAEQYKEQAEKGNAKVKQLKRQLEEAEEESQRINANRRKLQRELDEATESNEAMGRE
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56; Conser
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IPR004009;
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myosin_head.
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ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 159; DB 1
Pred. No. 0.095;
2; Mismatches
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COILED COIL (POTENTIAL).
CARBOXYL-TERMINAL.
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029230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=VC-16 / DSM 4304 / ATCC 49558; MEDLINE=98049343; PubMed=9389475;
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Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                    DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.

NP_BIND
38 AFF (BY SIMILARITY).

DOMAIN
148 728 COILED COIL (POTENTIAL).

SEQUENCE 886 AA; 103633 MW; D35641D499AA8B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003439;
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267
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SUBUNIT: FORMS a complex with mrell (By similarity).
SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and/or repositioning DNA ends into the mrell active
ERIED-LEKKAKEVKELKPKAERYSILEKLLSEINQALRDVEKREGDLTREAAGIQAQLK
                                                     DTLRDTLEERNATVESLQNALNK---AEMLCSTLKKQMKFLEQR------
                                                                                                                ESTREKTSEEAKNTESETKETEEHKSKTESTKKÖESSATÖEAKGTEEKTKETEKÖTKEAA
                                                                                                                                                                           KTIINKLFFDLAQEEENVLDAEFLKNELDSVKAQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro; IPR002017; Spectrin. PF00470; RecF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF1032;
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                                                                                                                                                                                                                                                                   Similarity
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Recf.
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Pred. No. 0.05
71; Mismatches
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                                                                                   Pfam; PF00612; IQ; 2.
Pfam; PF00613; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MLC-2).

(MLC-2).

(MLC-2).

(MLC-2).

(MLC-2).

(MLC-2).

(DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPERTITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES CYCLES OF A 28-RESIDUE REPEAT PATTERN. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILPIECE WHERE THE REGULATORY PHOSPHOXYLATION SITES RESIDE.

-!- MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHOXYLATION ON ENZYMATIC ACTIVITY.

-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle myosin heavy chain gene from Acanthamoeba: evidence of a hinge in the rodlike tail.";

J. Cell Biol. 105:913-925(1987).

-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

-!- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P05659;
01-NOV-1988
PROSITE; PS50096; IQ; Myosin; Coiled coil; Amposin; Alkylation; Alkylation
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000048;
InterPro; IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=87308395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Acanthamoebidae; Acanthamoeba. NCBI_TaxID=5755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myosin II heavy chain, non muscle.
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                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A27224; A27224.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y00624; CAA68663.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                               InterPro; IPR001609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRELDEEHRKN
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2d coil; Actin-binding; ATP-binding; Calmodulin-binding;
Alkylation; Phosphorylation; Multigene family.
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Best Local
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Sohda M., Misumi Y., Yano A., Takami N., Ikehara Y.;
"Phosphorylation of the vestcle docking protein pll5 regulates its
association with the Golgi membrane.";
J. Biol. Chem. 273:5385-5388(1998).

-i- FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR
INTERCISTERNAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR
TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICULES TO
THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY
INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR
AND TRACET MEMBRANES IN PROXIMITY (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES
BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDP_HUMAN
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pll5 (Transcytosis protein) (TAP) (Vesicle docking protein).
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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9; Mismatches
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ALKYLATION (SH-1)
PHOSPHORYLATION.
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W; 2CE49BE51173D17E
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Catarrhini; Hominidae,
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-HELICAL TAILPIECE
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RESULT 20
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Best Local S
Matches 64
                                                                                     01-NOV-1988
01-JUN-1994
16-OCT-2001
                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER;

PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS,

DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE;

PHOSPHORYLATED PROMOSTES DISSOCIATES,

PHOSPHORYLATION PROMOSTES DISSOCIATION.

SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
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                                                                                                                                                                                                       QDDLLVLLADQDQKILSLKNKLKD
                                                                                                                                                                                                                                                       VEGRLSALLQETKELKNEIKALSEERTAIKEQLDSSNSTIAILQTEKDKLELEITDSKKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                         QVAELKQELATLKSQLNSQSVEITKLQTEKQELLQKTEAFAKSVEVQGETETIIATKTTD
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1 (Rel. 40,
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S->A: LOSS OF PHOSPHORYLATION
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-89384556; PubMed-2506434;
George E.L., Ober M.B., Emerson C.P. Jr.;
George E.L., Ober M.B., Emerson C.P. Jr.;
"Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene are encoded by alternatively spliced exons.";
Mol. Cell. Biol. 9:2957-2974(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE Or . 41; Pundentline-87280141; Pundentline-87280141; Fundentline-87280141; Fundentline-87280141; Fundentline-87280141; Pundentline-87280141; Pundentline-872801415; Pundentline-872801415; Pundentline-872801415; Pundentline-872801415; Pundentline-872801415; Pundentline-872801415
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InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
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EMBL;
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                   ProDom; PD000355; myosin_head; SMART; SM00015; IQ; 1. SMART; SM00242; MYSC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.
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                                                                                     PRINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kronert W.A., Edwards K.A., Roche E.S., Wells L., Bernstein S.I., "Muscle-specific accumulation of Drosophila myosin heavy chains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                  InterPro;
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IL; M61229; AAA28687.1; A

IL; J02788; AAA28707.1; A

IL; J02788; AAA28707.1; A

IL; X60196; CAA42752.1; A

IL; X60196; CAA42753.1; A

IL; X60196; CAA42753.1; A

IL; X60196; CAA42754.1; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSIST
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBECLIULAR LOCATION: Thick filaments of the myofibrils.
ALTERNATIVE PRODUCTS: AS DROSOPHILA HAS A SINGLE MUSCLE MMCC ISOFORMS MUST RELY ON ALTERNATIVE RNA SPLICING THAT LE
DIFFERENCES IN THE C-TERMINUS OF THE VARIOUS MHC PROTEINS.
MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nberg D.R. II, Kronert W.A., O'Donnell P.T., Bernstein S.I.; ysis of the 5' end of the Drosophila muscle myosin heavy chain Alternatively spliced transcripts initiate at a single site and n locations are conserved compared to myosin genes of other
                                                                                                            PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
                                                                                                                                                          PF00063; myosin_head; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s requires a license agreement (S
an email to license@isb-sib.ch).
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IPR004009;
IPR002928;
IPR001609;
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MYSc;
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RESULT
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Best Local
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NP_BIND
VARSPLIC
VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2113
"A novel gene, AF-1p, fused to HRX in t(1:11)(p32 related to AF-4, AF-9 nor ENL."; Oncogene 9:1039-1045(1994).

-I- FUNCTION: INVOLVED IN CELL GROWTH REGULATION. SIGNAL TRANSDUCTION AND MITOGENICITY.
-I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-I- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
                                                                                                                                  "The human eps15 gene, encoding conserved in evolution and maps Oncogene 9:1591-1597(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2233
                                                                                                  SEQUENCE FROM N.A. MEDLINE=94181254;
                                                                                                                                                                 Wong W.T., Kraus M.H., Carlomagno F.,
Croce C.M., Huebner K., di Fiore P.P.;
                                                                                                                                                                                    TISSUE=Melanoma;
MEDLINE=94239734; PubMed=8183552;
                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                    Epidermal growth
                                                                                                                                                                                                                                                                                                                 01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                       01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                P42566;
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ATP-binding;
                                                                              Berger
                                                                                        Bernard
                                                                                                                                                                                                                                                                               EPS15 OR AF1P.
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                        204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KATGELA-----DRLK-----KDLVSS-RSKLKTLNTELDQAK-----LELRSAQKDLQ
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                                                                                        0.A.,
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59; Conservative
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
rowth factor receptor substrate 15
                                                                                                                                                                                                                                                                     (Human)
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                                                                                       254; PubMed=8134107; Mauchauffe M., Mecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Primates;
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. -> I (IN SHORT 1
MISSING (IN SUCCEX -> PF
MW.
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COILED (
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Pred. No. 0.21;
6; Mismatches
                                                                                        Mecucci
                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                              to 1p31-p32.
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RE (IN REF. 2).
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SIMILARITY).
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HSSP;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000261; EPS1
InterPro; IPR003903; UIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROGUE ACTIVATOR PROTEIN.
SIMILARITY: CONTAINS 1 EH DOMAIN.
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: PHOSPHORYLATED ON TYROSINE BY EGFR.
DISEASE: INVOLVED IN A T(1;11)(P32,Q23) CHROMOSOMAL TRANSLOCATION IN ACUTE LEUKEMIAS CAUSING FUSION TO THE TRITHORAX (MLL OR HRX) GENE PRODUCT WHICH CONTAINS DNA-BINDING MOTIFS RESULTING IN A ROGUE ACTIVATOR PROTEIN.
                                                                                                                                                                                                                              DLAQEEENVLD----AEFLK-NELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVE
STYEEELAKAREELSRLQQETAELEESVESGKAQLEPLQQHLQDSQQEISSMQMK
                                   KTLNTELDQA-----
                                                                  VQELLDELDEQKAQLE
                                                                                SLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRSE
                                                                                                                                                                                                  DRASLQKNIIGSSPVADFSAIKELDTLNNEIVDLQREKNNVEQDLKEKEDTIKQRTSEVQ
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Z29064; CAA82305.1;
P02633; IBOD.
                                                                                                                                                                                                                                                                        Similarity
53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00054; EFh; 3
SM00027; EH; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EF_HAND;
                                                                                                                                                                                                                                                                                                                                                         822
98673
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EPS15_repeat.
                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                     Score 154; DB:
Pred. No. 0.08;
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             -QRENTNLQK---
                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY TYR-K (POTENTIAL).

M -> I (IN REF. 2).

Alb9FB04A07FABEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
15 X 3 AA REPEATS OF D-P-F
                                                                                                                                                                                                                                                                                                                                                                                                                           PRO-RICH.
                     ---KLELRSAQKDLQSADQEITSLRKK
                                                                EQLKEVRKKCAEEAQLISSLKAELTSQESQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosomal translocation;
                                                                                                                                                                                                                                                                                                      ۳.
                                                                                                                                                                                                                                                                      60;
                                                                                                                                                                                                                                                                                                    Length 896
                                                                                                                                                                                                                                                                                                                                                                                                        TYR-KINASES)
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MRESULT 22
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DT 01-FEB
DT 16-OCT
DE MYOSIN
DE MYOSIN
DE MYOSIN
RA PHILLI
DA PHAM;
DA PH
                                                                                                                      PRINTS;
ProDom;
SMART; S
  Myosin;
Coiled (
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on different chromosomes.";
Circ. Res. 69:530-539(1991).
-!- FUNCTION: CELLILAR MYOSIN APPEARS TO I
CELL SHAPE, AND SPECIALIZED FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simons M., Wang M., McBride O.W., Kav
Gdula D., Adelstein R.S., Weir L.;
"Human nonmuscle myosin heavy chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phillips C.L., Yamakawa K., Adelstein R.S.; "Cloning of the cDNA encoding human nonmuscle myosin heavy analysis of human tissues with isoform-specific antibodies. J. Muscle Res. Cell Motil. 16:379-389(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYHA_HUMAN
P35580;
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004009; InterPro; IPR002928; InterPro; IPR002917; InterPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID-9606;
                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P08799;
MIM; 160776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; B61231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 63-722 FROM N.A MEDLINE=91316803; PubMed=18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-96025307; PubMed-7499478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B).
MYH10.
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000048;
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SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (ML REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEP CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEP CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                              PF00612; IQ; 1.
PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M69181; AAA99177.1;
; ATP-binding; Calmodulin-binding; Actin-binding; coil; Alkylation; Multigene family.

1 785 VOSIN HEAD-LIKE.
786 815 IQ.
                                                                                                                   ; PR00193; MYOSINHEAVY.
; PD000355; myosin_head;
SM00015; IQ; 1.
SM00242; MYSC; 1.
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                                                                                               PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pean Bioinformatics Institute. The
non-profit institutions as long
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Myosin_tail.
Spectrin.
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NP_BIND
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SEQUENCE
                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-89178677; PubMed-2926820;
Dibb N.J., Maruyama I.N., Krause M., Karn J.;
"Sequence analysis of the complete Caenorhabditis elegans heavy chain gene family.";
                                                                                                                                                                                                                                                                                            P02567; 019674;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Myosin heavy chain D (MHC D).
                            SEQUENCE OF 115-365 AND 1492-1763 I

MEDILINE-85201409; PubMed-3888374;

Karn J., Dibb N.J., Miller D.M.;

"Cloning nematode myosin genes.";

Cell Muscle Motil. 6:185-237(1985)
                                                                                             "Protein Structural domains in the Caenorhabditis elegans
"Protein Structural domains in the Caenorhabditis elegans
"Protein structural domains are not separated by introns.";
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[4]
SEQUENCE FROM N.A.
FRISTOL N2;
                                                                                                                              SEQUENCE OF 34-1795 FROM N.A. MEDLINE=83273600; PubMed=6576334;
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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64; Conservative
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21.0%;
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ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
MW; B2BB87FF35EA124F CRC64;
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on update)
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 EMBL; X08065; CAA30854.1; EMBL; M37232; AAA28120.1; EMBL; M37234; AAA28120.1; EMBL; Z71266; CAA95848.1; EMBL; Z71261; CAA95806.1; JEMBL; Z71265; CAA95806.1; JEMBL; Z71266; CAA95806.1; JPIR; S02772; MWKW1.
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pfam; pF02736; myosin_N; 1.
pfam; pF01576; myosin_tail; 1.
pRINTS; pR00193; MYOSINHEAVY.
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SMART; SM00242; MYSC;
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                                                                                                                                                                                                                                                                                                                           InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail
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 SEQUENCE
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CRC64;

128 700 710 710 94 94 98 98 98 97 39 39 39 1 39 408 474 474 577 681 1373 1659 1659 1659

METHYLATION (TRI-).

ALKYLATION (SH-1).

ALKYLATION (SH-2).

F -> E (IN REF. 2).

F -> E (IN REF. 2).

V -> D (IN REF. 4).

DV -> GD (IN REF. 4).

V -> D (IN REF. 4).

V -> G (IN REF. 4).

V -> G (IN REF. 4).

V -> G (IN REF. 2).

V -> G (IN REF. 2).

V -> G (IN REF. 2).

V -> G (IN REF. 3).

E -> Q (IN REF. 3).

S -> D (IN REF. 3).

846 846 1171 846 177

845 1938 1170 1938 1938 1938

ALPHA-HELICAL TAILPIECE (SHORT S2) LIGHT MEROMYOSIN (LMM). COILED COIL (POTENTIAL).

RODLIKE TAIL (S2 AND LMM DOMAINS)

MYOSIN HEAD-LIKE

ATP (BY SIMILARITY). ACTIN-BINDING.

682 778

myosin\_head;

Coiled coil; Thick filament; Actin-binding; n; Alkylation; Multigene family.

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CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MIC), 2 ALKALI LICHT CHAIN SUBUNITS (MLC) 2

CC -!- SUBCELLULAR LOCATION: THICK HILDSIVELY IN THE MYOFIBELLS.

CC -!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARYNCEAL MUSCLE.

CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CC -!- PIRSTIC FOR ALPHA-HELICAL COILED COILS.

CC -!- PIRSTIT FOR ALFALA HELICAL COILED COILS.

CC -!- PIRSTING CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED

SUBFRAGMENT (S2).

-!- SIBCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN UPAnyment.

C. ELEGANS.
entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gardner A., McMurray
Submitted (APR-1996)
                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN
                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Cervical carcinoma;

MEDLINE-93028466; PubMed-1409643;

MEDLINE-93028466; PubMed-1409643;

Garcia J.A., Ou S.-H.I., Wu F., Lusis A.J., Sparkes R.S., Gaynor R.

"Cloning and chromosomal mapping of a human immunodeficiency virus

"Cloning and chromosomal mapping of a human immunodeficiency virus

"TATA' element modulatory factor.";

"TATA' element modulatory factor.";

Proc. Natl. Acad. Sci. U.S.A. 89:9372-9376(1992).

-1- FUNCTION: THIS PROTEIN BINDS THE HIV-1 TATA ELEMENT AND INHIBI

TRANSCRIPTIONAL ACTIVATION BY THE TATA-BINDING PROTEIN (TBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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16-OCT-2001
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                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                  Transcription regulation;
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                        EMBL; L01042; AAD54608.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATA element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                      11 LAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTL---EERNATVESLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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AKLELRSAQKDLQSADQEITSLRKKSDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSLQDEMNSQDETIGKINKEKKLLEENNRQLVDDLQAEEAKQA--QANRLRGKLEQTLDE 1040
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                                                                                  Similarity 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
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                                                                                                                                                                                                                        984
1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
t modulatory factor (TMF).
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                    1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ormatics Institute. There are no restrictions on institutions as long as its content is in no attement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KEARKATGELADRLKKDLVSSRSK----
                                                                                                         14.2%;
                                                                                                                                                                                                                  Lion; DNA-binding; Repressor; Coiled
22 COILED COIL (POTENTIAL).
92 COILED COIL (POTENTIAL).
123170 MW; 26133E8E5F4677BE CRC64;
<u>...</u>
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                                                                                  49;
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                                                                          Pred. No. 0.11
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 153.5;
Pred. No. 0.
                                                                                                         Score 153; DB Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                  <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sparkes R.S., Gaynor R immunodeficiency virus
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                                                                          99;
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                                                                                                                                  Length 1093;
                                                                                                                                                                                                                                                                                                     Coiled
                                                                               Indels
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                                                                               34;
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L GENOMICS 54:188-189(1990).

C -!- FUNCTION: MUSCLE CONTRACTION.

C -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

C AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

C -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

C -!- SUBCELLULAR ECCATION: Thick filaments of the myofibrils.

C -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CC CHARACTERISTIC FOR ALPHA-HELICAL COTLED COILS.

CC C-PTM: TWO CYSTEINER RESIDUES IN THE 31 DOMAIN ARE SELECTIVELY ALXYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 25
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                    EMBL;
HSSP;
                                                        EMBL;
                                                                                          modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYHD_HUMAN
Q9UKX3; 095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The human extraocular muscle myosin heavy chain gene the cluster of fast and developmental myosin genes on Genomics 54:188-189(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99318869; PubMed-10388558; Weiss A., Schiaffino S., Leinwand L.A.; "Gomparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity."; J. Mol. Biol. 290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Extraocular muscle;
MEDLINE=99026150; PubMed=9806854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Winters L.M., Briggs M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Extraocular muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, extraocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1917-1938 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
                AF111782; AAD:
AF075248; AAC:
P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKQHRENIKKLNSMVERQEKDLGRLQVDMDELEEKNRSIQAALDSAYKELTDLHK 672
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                                     AAD29948.1; -. AAC83241.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schachat F.;
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603487;

InterPro;

IPR004009; IPR002928; IPR000048;

Myosin\_N. Į.

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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2:
MEDLINE-89178677; PubMed-2926820;
Dibb N.J., Maruyama I.N., Krause M., I "Sequence analysis of the complete Ca "Sequence analysis of the complete Ca heavy chain gene family.";
L. J. Mol. Biol. 205:603-613(1989).
C. -!- FUNCTION: MUSCLE CONTRACTION.
C. -!- SUBUNIT: MUSCLE MYOSIN IS A HEXALURANCE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 59
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P12844;
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01-OCT-1989
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pfam; pF02736; Myosin_N; 1.
pfam; pF01576; Myosin_tail; 1.
pfam; pF01576; MYOSINHEAVY.
pRINTS; pR00193; MYOSINHEAVY.
proDom; pD000355; myosin_head;
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Rhabditidae; Pelode
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SM00242; MYSc;
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59; Conservative
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myosin_head.
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(MHC A).
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24.9%;
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Caenorhabditis.
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ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (ST-1) (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

B MW; 1F6D006416381CD5 CRC64;
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COILED COIL (POTENTIAL).
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            HEXAMERIC PROTEIN THAT CONSISTS OF 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
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Caenorhabditis
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Matches 62
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InterPro: IPR001609; myosin_head
Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_Lail; 1.
PRINTS; PR00193; MYOSINHEAVY.
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DOMAIN
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ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                       1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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InterPro; IPR004009;
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 LKKEYENLKEARKATGELADRLKK---DLVSSRSKLKTLNT---ELDQAKLELRSAQKDL
                                     SNRKLNEDLQSEEDKVNHLEKIRNKLEQQMDELEENIDREKRSRGDIEKAKRKVE---GD
                                                                                                                                                     QATIDT------LRDTLEE---RNATVESLQNALNKAEMLCSTLKKQMKFLEQRQD
                                                                         ETKQAREEAHRLKCKMKTMEQIELLLQSQRSEVEEMI----RDMGVGQSAVEQLAVYCVS
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                                                                                                                                                                                                                                                                    62; Conservative
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myosin_head.
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ACTIN-BINDING.
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                Score 152; DB
Pred. No. 0.23
47; Mismatches
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THE RESULT OF THE PROPERTY OF 
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                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE SPLICING.
MEDLING-2051256; PubMed-11063258;
Chopra V.S., Metzler M., Rasper D.M.,
Singaraja R., Gan L., Fichter K.M., M.
Nicholson D.W., Hayden M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97285121; PubMed-9140394; Kalchman M.A., Kolde H.B., McCutcheon K., Graham R.K., Ni Kalchman K., Kazemi-Esfarjani P., Lynn F.C., Wellington Nishiyama K., Kazemi-Esfarjani P., Lynn F.C., Wellington Metzler M., Goldberg Y.P., Kanazawa I., Geitz R.D., Hayde "HIP1, a human homologue of S. cerevisiae Slazp, interact membrane-associated huntingtin in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat.
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"Genomic organization of
                                                                                                                                                                                                                                                               "HID12 is a non-proapoptotic member of an interacting protein with huntingtin. Mamm. Genome 11:1006-1015(2000).
-I- FUNCTION: MAY PLAY A FUNCTIONAL ROL
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1132
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MISCELLANGOUS: THE AFFINITY OF THE HUNTINGTIN PROTEIN-HIP1
INTERACTION IS INVERSELY CORRELATED TO THE LENGHT OF THE
INTERACTION IS INVERSELY TO THE HUNTINGTIN PROTEIN IN HUN
                                                                                                         SUBCELLULAR LOCATION: CYTOPLASMIC.
ALTERNATIVE PRODUCTS: 2 ISOFORMS;
BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY E
  POLYGLUTAMINE DISEASE.
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system.";
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TQEQLE-VLESLKQELATSQRELQVLQGSLETSAQSEANWAAEFAELEKERDSLVSGAAH
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                     DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete NP_BIND 30 37 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00470; RecF; 1. SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA double-strand break repair rad50 RAD50 OR PAB0812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Forms a complex with mrell (By similarity). SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
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een the Swiss Institute of Bioinfo
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-QRQDETKQAREEAHRLKCKMKTM---EQIELL--LQSQRS 123
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                                                                                                                                                                                                                                                   57;
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COILED COIL (POTENTIAL).
MW; FDB177EC7E026479 CRC64;
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Pred. No. 0.11
57; Mismatches
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                                                                                                                                                                                                                                                                                                                                       OF PARAMYOSIN.";

1. MOI. BIOI. 207:451-454(1989).

2. I. MOI. BIOI. 207:451-454(1989).

2. I. MOI. BIOI. 207:451-454(1989).

2. I. MORTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT OF MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES.

2. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

2. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

3. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

4. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

4. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

5. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

5. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

5. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

6. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

6. I. SUBUNIT: HOMODIMER (BY SIMILARITY).

6. I. MANY THICK FILAMENT (BY SIMILARITY).

7. I. MANY THICK FILAMENT (BY SIMILARITY).

8. I. M
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01-JUL-1989
15-JUL-1998
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Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kagawa H., Gengyo K., McLachlan A.D., Brenner S., Karn J.; "Paramyosin gene (unc-15) of Caenorhabditis elegans. Molecular cloning, nucleotide sequence and models for thick filament
                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kagawa H., Gel
J. Mol. Biol.
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                                                                                                                                         entities requires a
                                                                                                                                                          modified and this statement
                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schriefer L.A., Waterson R.H.; "Phosphorylation of the N-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89329026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
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                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collab meen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                       s04027; s
                                                                                                                                                                                                                                                                                  SIMILARITY: HIGH,
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                                    P80220;
                                                                                                                 s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATED ON SERINE
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bl. 211:665-665(1990).
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MEDLINE=98037449; PubMed=9371398;

Kondoh N., Nishina Y., Tsuchida J., Koga M.,

Inazawa J., Taketo M., Nozaki M., Nojima H.,

Okuyama A., Nishimune Y.;

"Assignment of synaptonemal complex protein"

"Assignment of synaptonemal complex protein"
chromosome 1p13 by fluorescence in situ hybridiza expression in the testis.";
Cytogenet. Cell Genet. 78:103-104(1997).
-i- function: major component of the transverse formation: major component of the transverse function: major complexes (SCS), formationeen chromosomes during meiotic prophase.
-i- SUBCELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEME
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Mammalia; Eutheria; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNAPTONEMAL COMPLEX (BY SIMILARITY).
TISSUE SPECIFICITY: TESTIS.
DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF
FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS.
DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE
                                                                                                                                                                        NALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQ-----IELLLQSQRS
                                                                                                                                                                                                                                                                 DLAQEEENVLDAEFLKN-ELDSVKAQLSQKDRE-KRDSQAIIDTLRDTLEERNATVESLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602162;
KISEENLLEEVEKAKVIADEAVKLQKEIDKRCQHKIAEMVALMEK
                                   RSKLKTLNTELDQAKL---ELRSAQKDLQSADQ----EITSLRKK
                                                                        YIEELQQENKALKKKGTAES--KQLNVYEIKVNKLELELESAKQKFGEITDTYQKEIEDK
                                                                                                             EVEEM----IRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSS
                                                                                                                                                 RMLKQIENLQETETQLRNELEYVREELKQKRDE----VKCKLDKSEENCNNLRKQVENKNK
                                                                                                                                                                                                                             DLKTELEN---
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D67035; BAA22586.1;
                                                                                                                                                                                                                                                                                                      . Similarity
59; Conser
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805
941
976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tein; Meiosis;

Colled coil.

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961 969

46 166

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                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                  MW.
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COLLED COIL (POTENTIAL).

RUCLEAR LOCALIZATION SIGNAL (F
NUCLEAR LO
                                                                                                                                                                                                                                                                                                  Score 150; DB 1
Pred. No. 0.14;
52; Mismatches
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2).

N -> I (IN REF. 2).

K -> T (IN REF. 2).

E -> D (IN REF. 2).

P -> S (IN REF. 2).

P -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQLTAITTSEQYYSKEVKDLKTELENEK -> YSYCHYHKW TVLPKRGQRPKLSSKRE (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                      86;
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                                                                                                                                                                                                                                                                                                                                       Length 976;
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(POTENTIAL).
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in no way
commercial
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RESULT 31
MYHB_HUMAN
ID MYHB_H AC
P13535
DT 01-JAN
DT 15-JUL
DT 16-OCT
DE MYSS.
OC EUMARY
OC MAMBILIN
RN [1]
RN [2]
RN [2]
RR SEQUEN
RC FISSUE
RX KARSchel
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RT Genez
RT TGenez
RT TGenez
RA Stedma
RT TGenez
RT TGe
                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-90323631; PubMed-2373371;
MEDLINE-90323631; PubMed-2373371;
Karsch-Mizrachi I., Feghali R., Shows T.B. Jr., Lein
Karsch-mizrachi G a full-length human perinatal myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYH8_HUMAN STANDARD; PKT; 19
P13535; Q14910;
D1-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myosin
Eur. J
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-46 FROM N.A. Esser K., Tidhar A., Myszk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 860-1937 FROM N.A. MEDLINE=89234168; PubMed=2715179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Skeletal muscle; MEDLINE-90235862; PubMed-1691980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of a transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Skeletal muscle;
MEDLINE=95324556; PubMed=7601129;
MEDLINE E.H., Kelly A.M., Pompido
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Generation of a full-length human encoding cDNA."; Gene 89:289-294(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arnold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 502-1937 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stedman H.H.,
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"Molecular genetic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of three developmentally controlled isoforms of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                   MEROMYOSIN (LMM) AND 1 HEAVY PROPERTY FURTHER INFO 2 GLOBULAR SUBFRAGMENT (S2).

SIMILARITY: CONTAINS 1 MYOSIN-SIMILARITY: CONTAINS 1 IQ DOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            perinatal myosin heavy chain.";
ll Biol. 108:1791-1797(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. 230:1001-1006(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. 189:55-65(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human perinatal myosin heavy-chain
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                                                                                                                                 MYOSIN-LIKE GLOBULAR IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Braun
  removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a
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on update)
, perinatal (MyHC-perinatal).
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osin heavy-chain-
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                                                                    1439
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HSSP; P08799; 1LVK.
MIM; 160741; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z38133; CAA86293.1; -.
EMBL; X51592; CAA35941.1; -.
EMBL; M35250; AAA36346.1; -.
EMBL; AF067143; AAC21557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin; Muscle protein; C ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; pF00063; myosin_head; 1.
pfam; pF02733; myosin_n; 1.
pfam; pF01576; myosin_tail; 1.
pfam; pF01593; mYOSINHEAVY;
                                                                                                                                                                                                                                                                         1272 LINDL---TAQRARLQTEAGEYSRQLDEKDALVSQLSRSKQASTQQIEELKHQLEEETKA 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO
Pfam; PF00612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                194
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ETLRRENKNLQ----
                            E-LRSAQKDLQSADQEITSLRKK
                                                                 NAACAALDKKQRNFDKVLSEWKQKYEETQAELEASQKESRSLSTELFKVKNVYEESLDQL 1498
                                                                                                                                                                        TKQAREE-AHRLK----
                                                                                                                                                                                                      KNALAHALQSSRHDCDLLREQYEEEQEGKAELQRALSKANSEVAQWRTKYETDAIQRTEE
                                                                                                                                                                                                                                          VESTQNALNKAEMLCSTLKKQMKFLE---
                                                                                                   AVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLNTELDQAK--
                                                                                                                                   LEEAKKKLAQRLQEAEEHVEAVNAKCASLEKTKQRLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M36769; AAC17185.1;
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                     970
1072
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1504
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1914
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781
842
181
658
760
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698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
970
1072
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1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           780
813
1937
188
680
774
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708
QEISDLTEQ 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQ.
Myosin_N.
Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                14.0%;
24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                   222762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coiled coil; Thick filan
n; Alkylation; Multigene
                                                                                                                                                       ----CKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQL 142
                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                            Score 150; DB
Pred. No. 0.29
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQ.
COILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYOSIN HEAD-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thick filament; Actin-binding;
; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                DВ
. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                     -NEVEDLMLD
                                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                                             Length 1937;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                              66;
                                                                                                                                                                                                                                         -QRQDE 93
                                                                                                                                     VERS
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                   193
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RESULT OF STATE OF ST
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                                                                                                  Query Match
Best Local
                                                                           Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.;

SUBMITTED (JUL-1995) to the EMBL/GenBank/DBJ databases.

SUBMITTED (JUL-1995) TO THE EMBL/GenBank/DBJ databases.

TO FLAY A ROLE IN CYTC

CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWI
                                                                                                                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAT
                                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOm; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002928; Myosin_tail
InterPro; IPR001609; myosin_head
Pfam; PF00612; IQ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, List sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---
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                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                       10 DLAQEEENVL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION CAPPING.
CAPPING.
SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2).
ENGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPCHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                           l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                         coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00015;
                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Calmodulin-binding; coil; Alkylation; Multigene family
                                                                                                                                                                                                                        ; Alkylation; Multigene f.
1 778 MYOSIN
779 808 IQ.
841 1927 COILED COILED ATP (PO)
654 676 ACTIN-B
694 694 ALKYLAT
704 704 ALKYLAT
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYSc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQ;
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A
-DAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVES
                                                                                                  14.0%;
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin_N.
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                                                                           44;
                                                                                                                                                                                   IQ.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
6 MW; 9B9876D9681FB19E CRC64;
                                                                                                Score 150; DB Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                              MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1961
                                                                                                                                                                                                                                                                                                                                                                                                                             Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA
                                                                                                                       1;
                                                                        96;
                                                                                                                          Length 1961;
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S OF 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEPTAPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOKINESIS
                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAVY
AND 2
                                                                        Gaps
                          65
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RESULT 33
MYSS_CYPCA
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                                                                                                                                                                                                                                                                              Hirayama Y. Watabe S.;

**Structural differences in the crossbridge head of temperature-

**The content of the crossbridge head of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Actinopterygii; Neopterygii; Teleostei, Cypriniformes, Cyprinidae, Cyprinus. NCBI_TaxID-7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1345
                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1387-1528 FROM N.A. MEDLINE=95194396; PubMed=7887920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acclimation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97176447; PubMed=9023993;
Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
"cDNA cloning of myosin heavy chain isoforms from carp fast skeletal muscle and their gene expression associated with temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fast muscle;
MEDLINE=97352533; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYSS_CYPCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1228 ELANEVKALLQGKGDSEHKRKK----VEAQLQELQVKFSEGERVRTELADKVSKLQVELDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watabe S., Imai J., Nakaya M., Hirayama Y.,
Uozumi T., Hirono I., Aoki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                       PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLAMEDUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

SUBFRAGMENT (S2).

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SWISS-PROT entry
een the Swiss Ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTGLLNQSDSKSSKLTKDFSALESQLQDTQELLQEENRQKLSLSTKLKQMEDEKNSFREQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  981-1935 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200:27-34(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9208928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -EKQIATLHAQVTDMKKKMEDGVGCLETAEEAKRRLQKDLEGLSQR 1401
is copyright. It is produ
stitute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Euteleostei;
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                     produced through a collaboration
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Best Local 9
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Pfam; PF00613; Myosin_head; 1.

Pfam; PF02736; Myosin_kai; 1.

Pfam; PF02736; Myosin_tai; 1.

Pfam; PF01576; Myosin_tai; 1.

Pfam; PF01576; Myosin_head; 1.

PRINTS; PR00193; MYOSIN_head; 1.

SMART; SM00015; IQ; 1.

SMART; SM00242; MYSC; 1.

PROSITE; PS50096; IQ; 1.

PROSITE; PS50096; IQ; 1.
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Pfam; PF0
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EMBL;
MYH9_HUMAN STANDARD; PRT; 1960 AA.

p35579; O60805;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain,
type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A).
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D50476; BAA09069.1;
D43700; BAA07802.1;
P08799; IMMD.
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IPR004009; Myosin_N.
IPR002928; Myosin_tail.
IPR001509; Myosin_head.
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Pred. No. 0.33;
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ALKYLATION (SH-2).
ALKYLATION (SH-2).
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RX MDLINE 20037165; PubMed-10591208;
RX MDLINE 20037165; PubMed-10591208;
RA Llamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,
RA Bagyley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
RA Blakey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,
RA Coville G.J., COX A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., COX A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., COX A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., COX A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., COX A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., COX A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., COX A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., COX A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA RIBERT M. M., Hall C., Hall R., Hall Tamlyn G.,
RA RIBERT M. M., MINIMAN M., RAILL TAMLYN G.,
RA RIBERT M. M., William S., Hall Tamlyn G.,
RA RILOY G., Lloyd D.M., Martin G.K., Langford C.F., Leversha M.A.,
RA Mathews L., McCann O.T., McClay J., McLaren S., Mcmurray A.A.,
RA Mathews L., McCann O.T., McClay J., McLaren S., Mcmasay H.,
RA Ramsey Y., Rogers L., Ross M.T., Sockt C.E., Sehra H.K., Skuce C.D.,
RA Milne S.A., Mortimore B.J., Phillips S.H., Plumb R.W., Ramsay H.,
RA Ramsey Y., Rogers L., Ross M.T., Sockt C.E., Sehra H.K., Skuce C.D.,
RA Milner T.E., Williams L., Williams S., Williams
      Toothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M. Arnaout M.A., Clayton L.K., Tenen D.G.;
"Cellular myosin heavy chain in human leukocytes: isolation of 5', cDNA clones, characterization of the protein, chromosomal localization, and upregulation during myeloid differentiation."; Blood 78:1826-1833(1991).
SEQUENCE OF 714-1960 FROM N.A. MEDLINE=90138958; PubMed=1967836; MEDLINE=90138958; PubMed=1967836; Saez C.G., Myers J.C., Shows T.B., Leinwand L.A.; "Human nonmuscle myosin heavy chain mRNA; generat through alternative polyadenylylation.";
                                                                                                                               Circ.
                                                                                                                                                                      MEDLINE=91316803; PubMed=1860190;
Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa
Gdula D., Adelstein R.S., Weir L.;
"Human nonmuscle myosin heavy chains are encoded by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature
                                                                                                                                                      on different chromosomes.";
                                                                                                                                                                                                                                                             SEQUENCE OF 1-715 FROM
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                                                                                                                                                                                                                                                               N.A.
                      generation
                        of
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CAPPING:
CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2
REGULARORY LIGHT CHAIN SUBUNITS (MLC-2).

POMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILE.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL FOR ANY HEGGLIN ANOMALY
MAND AND AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED
BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUCOCYTE INCLUSIONS.

WITH ADDITIONAL ALPORT LIKE CLINICAL FEATURES OF SENSORINEURAL
DEAFNESS, CATARACTS AND NEPHATIS.

CIBSS, AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED
BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUCOCYTE INCLUSIONS.

CHARACTERIZED BY PROGRESSIVE HEARING OF AN AUTOSOMAL DOMINANT FLATELETS AND LEUCOCYTE INCLUSIONS.

CHARACTERIZED BY PROGRESSIVE HEARING INPAIRMENT AND
COCHLEOSACCULAR DEGENERATION.

COCHLEOSACCULAR DEGENERATION.

COCHLEOSACCULAR DEGENERATION.

COCHLEOSACCULAR DEGENERATION.
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                                                                                                                                                                                                                                                                                                  the
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MEDLINE=20428192; PubMed=10973259;

Seri M., Cusano M., Gangarossa S., Caridi G., Bordo D., Lo Nigro C Ghiggeri G.M., Ravazzolo R., Savino M., Del Vecchio M., d'Apolito Iolascon A., Zelante L.L., Savoia A., Balduini C.L., Noris P., Magrini U., Belletti S., Heath K.E., Babcock M., Glucksman M.J., Maliprandis E., Bizzaro N., Desnick R.J., Martignetti J.A.;
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[7]
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Nat. Genet. 26:103-105(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS MHA ILE-1155 AND LYS-1841.
MEDLINE=20428193; PubMed=10973260;
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Lalwani A.K., Goldstein J.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mutations in MYH9 result in the May-Hegglin anomaly, and Fechtner and
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                                                                                                        782215; CABO5105.1;

7881105; AAA559888.1;

7869180; AAA61765.1;

789180; AAA61765.1;

7991013; AAA33349.1;

7908799; 1LVK.
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dstein J.A., Kelley M.J.,
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Coiled coil;
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Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PTCDDom; PD000355; myosin_head;
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                                     182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00612; IQ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                               90
                                                                                                                                                   39
                                                                                                                                                                                        4 INKLFFDLAQEEENV-----
KKSDD
                 QDTQELLQEENRQKLSLSTKLKQVEDEKNSFREQLEEEEEAKHNLEKQIATLHAQVADMK
                                                       EAQLQELQVKFNEGERVRTELADKVTKLQVELDNVTGLLSQSDSKSSKLTKDFSALESQL
                                                                          EEMIRDMGV---
                                                                                                            RQ------QIELLLQS-----QRSEV 125
                                                                                                                                EKQKRDLGEELEALKTELEDTLDSTAAQQELRSKREQEVNILKKTLEEEAKTHEAQIQEM 1190
                                                                                                                                                  DREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKK------QMKFLEQ
                                                                                            RQKHSQAVEELAEQLEQTKRVKANLEKAKQTLENERGELANEVKVLLQGKGDSEHKRKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002928;
IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR004009;
                                                                                                                                                                                                                                                                 53
660
869
931
1240
1350
1764
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                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 779
837
174
654
694
704
                                                                                                                                                                                                                                                                                                                                                                                                                                               702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alkylation;
                                                                                                                                                                                                                                                       55
660
869
931
1241
1250
1350
1764
1771
A; 226531
                                                                        -GQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKL 181
                                                                                                                                                                                                                                                                                                                                                                                                         1155
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                                 TLNTELDQAKLELRSAQKDLQSADQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin_N.
Myosin_tail.
Spectrin.
                                                                                                                                                                                                                 13.9%;
19.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calmodulin-binding; Actin-binding;
ion; Multigene family; Disease muta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myosin_head
                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                     KG -> GR (IN REF. 4).
E -> EE (IN REF. 2).
T -> A (IN REF. 2).
S -> G (IN REF. 2).
                                                                                                                                                                                                                                                        Œ;
                                                                                                                                                                                                                                                                                                    EAI -> RGH (IN REF. T -> S (IN REF. 3).
T -> M (IN REF. 4).
C -> Y (IN REF. 4).
                                                                                                                                                                                                                                                                                                                               /FTId=VAR_010796.
E -> K (IN MHA).
FTId=VAR_010797.
EAI -> RGH (IN RE)
                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_010794.
R -> C (IN SBS).
/FTId=VAR_010795.
                                                                                                                                                                                                                  Score 149;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N -> K (IN MHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALKYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_010793.
                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_010792
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VAR_010791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALKYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COILED COIL (POTENTIAL)
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           -> I (IN MHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                     H (IN FTNS)
                                                                                                                                                                                                                                                                                                                                                                                                                            H (IN DFNA17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN FTNS)
                                                                                                                                                                                       -----LDAEF--LKNELDSVKAQLSQK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SH-1) (POTENTIAL). (SH-2) (POTENTIAL).
                                                                                                                                                                                                                  DB 1;
.33;
                                                                                                                                                                                                         87;
                                                                                                                                                                                                                           Length 1960;
                                                                                                                                                                                                                                                        CRC64
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation;
                                                                                                                                                                                                        90;
                                    -EITSLR
                                                                                                                                                                                                        Gaps
                                                       1310
                                                                                            1250
                                    213
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10;

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NYHB_CHICK
ID MYHB_CHICK
AC P1058_C
AC ACLOSS
OC Eukryy
OC Archos
OC Eukryy
OC Archos
OC Eukryy
OC Archos
OC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                              RT pre-power stroke state.";

Cell 94:559-571(1998).

CC -!- FUNCTION: MUSCLE CONTRACTION.

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: THE REPUBLICAL COLLED COLLS.

CC -!- SUBCELLULAR COCATION: THE SI DOMAIN ARE SELECTIVELY

CC -!- PIM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

CC -!- MISCELLANEOUS: BACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain deduced from its complementary DNA sequence. Implications topography and function of myosin.";
J. Mol. Biol. 198:143-157(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myosin heavy chain, gizzard smooth muscle.

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P1058/;
01-JUL-1989 (Rel. 11, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                     use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dominguez R., Freyzon Y., Trybus K.M., Cohen C.; "Crystal structure of a vertebrate smooth muscle myosin motor and its complex with the essential light chain: visualization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (3.5 ANGSTR MEDLINE-98412652; Pubmed-9741621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maita T., Onishi H., Yajima E., Matsuda G., "Amino acid sequence of the amino-terminal heavy chain of chicken gizzard myosin."; J. Biochem. 102:133-145(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=88118918; PubMed=2892941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYHB_CHICK
P10587;
                                                            EMBL; X06546; CAA29793.1;
                                                                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masaki T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yanagisawa M., Hamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete primary structure of vertebrate smooth muscle myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                    SUBFRAGMENT (S2).
SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKMED
                                   S03166;
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                                      S03166
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                                                                                                                                                                                                                                                                                                                                                                        1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
1 IQ DOMAIN.
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MYSU_RABIT
ID MYSU_R
AC Q99105
AC Q99105
DT 01-JUN
DT 15-JUL
DE Myosin
OS Orycto
OC Eukary
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
RC TISSUE
RX MEDLIN
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Best Local Similarity
                                                                                      01-JUN-1994 (Rel. 29
01-JUN-1994 (Rel. 29
15-JUL-1998 (Rel. 36
Myosin heavy chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
MOD_RES
MOD_RES
CONFLICT
CONFLICT
SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC;
PROSITE; PS50096; IQ;
                                                                                                                                     MYSU_RABIT
Q99105;
                                                                                                                                                                                                                                                     1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02736; MyOsin_N; 1.
Pfam; PF01576; MyOsin_Lail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
 MEDLINE=91139672;
           SEQUENCE FROM
TISSUE=Fetal a
                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                            Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                        1055 RQELEKIKRKLEGESSDLHEQIAELQAQIAELKAQLAKKEEE 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Methylation; Alkylation; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001609;
Pfam; PF00612; IQ; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002928;
InterPro; IPR002017;
                                           NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
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                                                                                                                                                                                                                                                                                                                                            892
                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                 14 EEENVLDAEF ----- LKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQN
                                                                                                                                                                                                                             RSKLKTLNTELDQAKLELRSAQKDLQSADQEI-TSLRKKSDD 218
                                                                                                                                                                                                                                                     LTKERKLLEERVSDLTTNLAEEEEKAKNLTKLKNKHESM-----ISELEVRLKKE-EKS
                                                                                                                                                                                                                                                                                                RSQQLQAEKKKMQQQMLDLEEQLEEEEAARQKLQLEKVTADGKIKKMEDDILIMEDQNNK
                                                                                                                                                                                                                                                                                                                    ALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKC----KMKTMEQIELLLQSQ---
                                                                                                                                                                                                                                                                                                                                           EEKNLLQEKLQAETELYAEAEEMRVRLAAKKQE------LEEILHEMEARIEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1BR4;
                                                                                                                                                                                                                                                                         ----RSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tamily;
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    849
176
666
767
7127
716
                                                                                                                                                STANDARD;
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                                                                                               29, Created)
29, Last sequence update)
36, Last annotation update)
 PubMed=1995631;
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820
1978
1978
183
688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
127
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716
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781
                                                                                         embryonic smooth muscle
                                                       Lagomorpha;
                                                                   Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                    13.9%;
24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin_N.
Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myosin_head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                              228663 MW;
                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 149; DB Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN REF. 3).
KDTSITOGPSFS -> RTPASLKVHLFP (IN B7B6C923E5273D93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHYLATION (TRI-)
ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIN-BINDING BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COILED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RODLIKE TAIL
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                       Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COIL
                                                                                                                                                501
                                                                   Vertebrata;
                                                                                                                                                ΑA
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (S2 AND LMM DOMAINS).
                                                                                         isoform (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                        86;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 1978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REF.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                          177
                                                                                                                                                                                                                                                                                                1001
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RESULT
MFP1_AI
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AC QS
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                       MFP1_ARATH
Q9LW85;
16-OCT-2001
16-OCT-2001
16-OCT-2001
MAR binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                         MFP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - -
      Arabidopsis
                                                                                                                                                                   ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002928; Myosin_tail.
Pfam; PF01576; Myosin_tail; 1.
Myosin; Muscle protein; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscle and its expression during vascular development and
arteriosclerosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsuchimochi H., Yazaki Y., Ohkubo A., Takaku F.;
"cDNA cloning of a myosin heavy chain isoform in embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuro-0 M.,
                                                                                                                                                                                                                                                                                                                                150
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                                                                                                                                                                                                                                                                                                                                                                                                             90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: MUSCLE CONTRACTION.

SUBBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MIC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2),
SUBCELLULAR LOCATION: Thick filaments of the myofibrils. SHOWING
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEDTAPEDTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFRAGMENT (S2).
SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONSERVED.
                           OR AT3G16000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A38650;
                                                                                                                                                                                                                                                                                                                            DLKDLEAQIEAANK---ARERRVKQLRRLQAQMKDYQRELEEARGSRDEIFAQSKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEMLCSTLKKQMKFLEQRQDE-----TKQAREEAHRLKCKMK----TMEQIEL 116
                                                                                                                                                                                                                                              SEKKLKSLEAEILQLQEELASSERARRHAEQE
                                                                                                                                                                                                                                                                                      SRSKLKTLNTELDQAKLELRSAQKDLQSADQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNKQLRADMEDLMSSKDDVGKNVHELEKSKRALEQQVEEMRTQLEELEDELQATEDAKLR
                                                                                                                                                                                                                                                                                                                                                                   LLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVS
                                                                                                                                                                                                                                                                                                                                                                                                             LEVNTQAMKAQFERDLQARDEQSEEKKRLLTKQVRELEAELEDERKQRALAVASKKKMEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
ol (Rel. 40, Createg)
Ol (Rel. 40, Last sequence update)
Ol (Rel. 40, Last nonotation update)
ng filament-like protein 1.
ur3G16000 OR MSL1.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagai R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501
457
58118 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 148.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RODLIKE TAIL (S2 AND LMM DOMAINS)
COILED COIL (POTENTIAL).
; 49F793247D00973E CRC64;
                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                              727
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                                                              update)
                                                                                                                                                                                                                                                234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           149
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      OCC OCC DTT DTC
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Best Local
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                        XCAP-C
                                                                                                                           Chromosome
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                                                                                                                                                                                                                             XCPC_XENLA
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P50532;
01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
15-JUL-1998 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    features of the regions of 4,304,004 by control of clones.";
DNA Res. 7:131-135(2000).

-i- FUNCTION: BINDS DNA. INTERACTS WITH CHROMATIN VIA MATRIX
-i- FUNCTION: BINDS CONNECTING CHROMATIN WITH THE NUCLEAR ATTACHMENT REGIONS (MARS). LIKELY TO PARTICIPATE IN NUCLEAR ARCHITECTURE BY CONNECTING CHROMATIN WITH THE NUCLEAR MATRIX POTENTIALLY WITH THE NUCLEAR MATRIX (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: NUCLEAR MATRIX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S "Structural analysis of Arabidopsis thaliana chromosome 3. I. St features of the regions of 4,504,864 bp covered by sixty P1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiderrosids II; Brassicales; Brassicaceae; Arabidopsis.
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Me
                                                     Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB012247; BAB02666.1; -
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nes 55; Conser
                                                                                                                                                                                                                                                                                                                                                                  KDKVADLTEKYED
                                                                                                                                                                                                                                                                                                                                                                                                                     DQEITSLRKKSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collai
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQNALNKA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENSLSKAGEDKEALETKLREKLDLVEGLQDRINLLSLELKDSEEKAQRFNASLAKKEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; DNA-binding;
140 692 (
                                                                                                      assembly protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       727 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ARKATGELADRLKKDLVSSR-SKLKTLNTELDQAKLELRSAQKDLQSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMLCSTLKKQMKFLEQRQD - - - - - - ETKQAREEAHRLKCKM - - - - - -
                                                                                                                        34, Created)
34, Last sequence update)
36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                                                                                                   218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
  n; Craniata; Ve
Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 148.5; D
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-SER.
5F4F9A0F7F623CAA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coiled coil.
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                       1290
                                                                                                                                 update)
  Vertebrata;
ia; Pipoidea;
                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
  Euteleostomi;
; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ALDDVNKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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and TAC
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RESULT 39
REST_HUMAN
ID REST_HUMAN
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Best Local S
Matches 63
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NP_BIND 107 114

DOMAIN 264 594

DOMAIN 764 1027

DOMAIN 1094 1129

DOMAIN 1263 1290

DOMAIN 263 1290

DOMAIN 747 750

DOMAIN 747 750

DOMAIN 841 844
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InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as modified and this statement is not removed. U entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      condensation in vitro.";
Cell 79:449-458(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U13673; AAA64679.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A heterodimeric coiled-coil protein required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95042742; PubMed=7954811;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hirano T.,
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                                                                            511
                                                                                                                                                     140
                                                                                                                                                                              394
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                                                                                                                                                                                                                                                                              284 MVEKEKDALEGEKNKAIEFLTVENETFKKKNQLCQYYIHDLQKRSRDKEAQKEKIQEDTK
                                                                                                                                                                                                    97
                                                                                                                                                                                                                                                      47
                                                                                                                                                                                                                                                                                                     11 LAQEEENVLDA-----EFL--KNELDSVKAQL------SQKDREKRDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOTIC CHROMOSOMES.
SUBUNIT: ASSOCIATES MITH XCAP-E PROBABLY AS HETERODIMER.
SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN
MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND
FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.
DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL RECTIONS
DOMAIN: CONSISTS OF TWO PUTATIVE THE N- AND C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ween the Swiss Institute of Bioinfo
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: REQUIRED FOR BOTH ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                          AIID---TLRDTLEERNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQ------
                                                                          LSQLNKAKEALNTASATLKERRAAIKELETKLPKDEGD
                                                                                                                                          - EQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLNTELD-----
                                                                                                                                                                           TREKLKHSKSKVKKLQK----QLQKDKEKVDELKNVPANSQKIIAEETNKKDLLEKQKEKE
                                                                                                                                                                                                    AREEAHRLKCKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAV------
                                                                                                                                                                                                                            DISEKSNTLLETMKEKNKALKDVEKQLNKI-----TKFIEENREKFTQLDLQDVD
                                                                                                                         EEKLKNVMDSLKKETQGLQEEKEVKEKELMEISKTVNEARSKMDVAQSELDIYLSRHNSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF02483; SMC_C;
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                   QAKLELRSAQ----KDLQSADQEI-TSLRKKSDD 218
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841
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              STANDARD;
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Coiled
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COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
POLY-PRO.
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Pred. No. 0.
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W; 2931249924FE90F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ALA.
              PRT;
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear
              1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Peripheral blood monocytes;
MEDLINE-92289675; PubMed-1600942;
Bilbe G., Delabie J., Brueggen J., Richener
Cerletti N., Sorg C., Odink K., Tarcsay L.,
de Wolf-Peeters C., Shipman R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Restin (Cytoplasmic linker protein 170 alpha-2) (CLIP-170) (Reed-
                                                                                                                                                                                                                        VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-92405160; PubMed-1356075;

MEDLINE-92405160; PubMed-1356075;

Pierre P., Scheel J., Rickard J.E., Kreis T.E.;

"CLIP-170 links endocytic vesicles to microtubules

Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Restin: a novel intermediate filament-associated perpressed in the Reed-Sternberg cells of Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01302; CAP_GLY; 2. SMART; SM00343; ZnF_C2HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X64838; CAA46050.1; EMBL; M97501; AAA35693.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOSKELETON.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 11:2103-2113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00845; CAP_GLY_1; PROSITE; PS50245; CAP_GLY_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000938;
InterPro; IPR001878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 179838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S22695; S22695
                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF HODGKIN'S DISEASE.
                                               NKLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREK-----
NMLSSDLEKLRENLADMEAKFREKDEREEQLI-KAKEKLENDIAEIMKMSGDNSSQLTKM 936
                                                                                                   l Similarity
54; Conser
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microtubules;
                                                                                                                                                                                                                           1069
A; 160989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAP-Gly.
Znf_CCHC
SLY; 2.
                                                                                                                          23
                                                                                                                        . 98
                                                                                                                                                                                                                      S; Coiled coil; Repeat; Alternati
CAP-GLY 1.
SER-RICH.
CAP-GLY 2.
SER-RICH.
COILED COIL (POTENTIAL).
CCHC-BOX.
MISSING (IN SHORT ISOFORM).
MISSING (IN SHORT ESOFORM).
D -> E (IN REF. 2).
B 9 MW; 0A4F166DD94254E8 CRC64;
                                                                                                   38;
                                                                                                                        Score 148.5;
Pred. No. 0.
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                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                        . 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; Alternative splicing
                                                                                                                                               DB
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SPLICING.
THE REED-STERNBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H., Asselbergs F.A.M., Wiesendanger W.,
                                                                                                87;
                                                                                                                                               1;
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s disease.";
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P13540; 060540;
01-3AN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last seg
16-OCT-2001 (Rel. 40, Last anr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I- FUNCTION: MUSCLE CONTRACTION.
-I- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-I- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-I- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-I- SUBCELLULAR LOCATION: TALL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
-I- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
-I- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-I- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                             EMBL; L12104; AAA62313.1;
EMBL; X07273; CAA30256.1;
PIR; A28298; A28298.
HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang R., Sole M.J., Cukerman E., Liew C.-C
"Characterization and nucleotide sequence
"Characterization are most single sequence
heavy chain gene from Syrian hamster.";
J. Mol. Cell. Cardiol. 26:1155-1165(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=F1B; TISSUE=Liver; MEDLINE=95115033; PubMed=7815459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1038
                                InterPro;
                                                                   InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 16:4737-4737(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence of cDNA encoding the Syrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88247788; PubMed-3380703;
Jandreski M.A., Sole M.J., Liew C.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 962-1935 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDELRLKERDVEELQLKLTKANENASFLQKSIEDMTVKAEQSQQEAAKKH----
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      IPR004009;
IPR002928;
                                Myosin_N.
Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
ardiac muscle beta isofc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1934
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MOD_RES
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                                                                                                                                                                                                                                                                                                                1053 KLEGDLKLTQESIMDLENDKQQLDE---KLKKKDFELNALNARIEDEQALGSQLQKKLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001609; myosin_head. Pfam; PF00612; IQ; 2. Pfam; PF00063; myosin_head; 1. Pfam; PF02736; Myosin_N; 1. Pfam; PF01576; Myosin_tail; 1. PRINTS; PR00193; MYOSINHEAVY.
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SMART; SM00242; MYSC;
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SRQLDEKEALISQLTRGKLTYTQQLEDLKRQLEE 1320
                                        NTELDQAKLELRSAQKDLQSADQEITSLRKKSDD
                                                                                                                                                                                                                                       LQARIEELEEELEAERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQIEMNKKREAE
                                                                                                                                                                                                                                                                            RNATVESLQNALN------KAEMLCSTLKKQMKFLEQRQDE---------
                                                                                                                                                                                                                                                                                                                                                       KLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREK-----RDSQAIIDTLRDTLEE
                                                                               V---TSNMEQIIKAKANLEKMCRTLEDQMNEHRSKAEETQRSVNDLTSQRAKLQTENGEL
                                                                                                                    MGVGQSAVEQLAVYCVSLKKEYENLKE----ARKATGELADRLKKDLVSSRSKLKT----L
                                                                                                                                                         FQKMRRDLEEATLQHEATAAALRKKHADSVAELGEQIDNLQRVKQKLEKEKSEFKLELDD
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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177
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756
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                                                                                                                                                                                              -TKQAREEAHRLKCK-------MKTMEQIELLLQSQRSEVEEMIRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          779 MYC
809 IO
1934 CO
1934 ATI
184 ATI
676 ACT
770 ACT
128 MEE
1014 ALF
704 ALF
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1057 D
1057 D
1157 D
1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                              13.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alkylation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALKYLATION (SH-1) (POTEN

ALKYLATION (SH-2) (POTEN

D >> E (IN REF. 2).

T >> TE (IN REF. 2).

E -> Q (IN REF. 2).

L-> Y (IN REF. 2).

D-> Y (IN REF. 2).

L-> V (IN REF. 2).

D -> N (IN REF. 2).

D -> N (IN REF. 2).

C -> R (IN REF. 2).

T -> A (IN REF. 2).

C -> R (IN REF. 2).

C -> R (IN REF. 2).

C -> K (IN REF. 2).

M -> L (IN REF. 2).

M -> L (IN REF. 2).

M -> L (IN REF. 2).
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Pred. No. 0.35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIN-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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